



Sequence Listing

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ashkenazi, Avi J.
 - (ii) TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
 - (iii) NUMBER OF SEQUENCES: 28
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genentech, Inc.
 - (B) STREET: 1 DNA Way
 - (C) CITY: South San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94080
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WinPatin (Genentech)
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/993234
 - (B) FILING DATE: 19-NOV-01
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/828683
 - (B) FILING DATE: 31-MAR-1997
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/625328
 - (B) FILING DATE: 1-Apr-1996
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/710802
 - (B) FILING DATE: 23-Sep-1996
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Marschang, Diane L.
 - (B) REGISTRATION NUMBER: 35,600
 - (C) REFERENCE/DOCKET NUMBER: P1007P1D1
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650/225-5416
 - (B) TELEFAX: 650/952-9881
- (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 181 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Glu	Gln	Arg	Pro	Arg	Gly	Cys	Ala	Ala	Val	Ala	Ala	Ala	Leu
1				5					10					15
Leu	Leu	Val	Leu	Leu	Gly	Ala	Arg	Ala	Gln	Gly	Gly	Thr	Arg	Ser
				20					25					30
Pro	Arg	Cys	Asp	Cys	Ala	Gly	Asp	Phe	His	Lys	Lys	Ile	Gly	Leu
				35					40					45
Phe	Cys	Cys	Arg	Gly	Cys	Pro	Ala	Gly	His	Tyr	Leu	Lys	Ala	Pro
				50					55					60
Cys	Thr	Glu	Pro	Cys	Gly	Asn	Ser	Thr	Cys	Leu	Val	Cys	Pro	Gln
				65					70					75
Asp	Thr	Phe	Leu	Ala	Trp	Glu	Asn	His	His	Asn	Ser	Glu	Cys	Ala
				80					85					90
Arg	Cys	Gln	Ala	Cys	Asp	Glu	Gln	Ala	Ser	Gln	Val	Ala	Leu	Glu
				95					100					105
Asn	Cys	Ser	Ala	Val	Ala	Asp	Thr	Arg	Cys	Gly	Cys	Lys	Pro	Gly
				110					115					120
Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	Gln	Cys	Val	Ser	Ser	Ser	Pro
				125					130					135
Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	Gly	Ala	Leu	His	Arg	His
				140					145					150
Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	Asp	Thr	Asp	Cys	Gly	Thr	Cys
				155					160					165
Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys	Val	Ser	Cys	Pro
				170					175					180

Thr

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 433 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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CTGCTGGGGG CCCGGGCCAG NGGCGGCACT CGTAGCCCCA GGTGTGACTG 50
TGCCGGTGAC TTCCACAAGA AGATTGGTCT GTTTTGTTGC AGAGGCTGCC 100
CAGCGGGGCA ACTACCTGAA GGCCCCCTGC ACGGAGCCCT GCGCAACTCC 150
ACCTGCCTTG TGTGTCCCCA AGACACCTTC TTGGCCTGGG AGAACCACCA 200
TAATTCTGAA TGTGCCCGCT GCCAGGCCTG TGATGAGCAG GCCTCCCAGG 250
TGGCGCTGGA GAACTGTTCA GCAGTGGCCG ACACCCGCTG TGGCTGTAAG 300
CAGGGCTGGT TTGTGGAGTG CCAGGGTCAG CCAATGTGTC AGCAGTTTCA 350

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CCCTTCTAAT GCCAACCATG CCTAGACTGC GGGGCCCTGC AACGCAACAC 400
ACGGCTAATN TGTTTCCCGC AGAGATNATT GTT 433

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCGCTGCCA GGCCTGTGAT GAGCAGGC 28

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGGGCCCCG CAGTCTAGGC ATGGTTGG 28

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1438 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGGC GCGGAGGCCG AGAGAGAAGT CACTTGCCCT GGCTCTACCT 50
TGAAGTGGTT CTCAGGGTTG GGGCGAGAGT CGGGGTGGGG ACCGAGATGC 100
AGCTCTATCC TGTGCCCTG GTCGCAGCAG GCAGCCCAGC GCTTCGCGTG 150
TTCTACTTGG CCTGTCCGCT GCCGCCTAAT GAGCTCAGGT CTAGGCCGAG 200
CAGAGGGGGC ACCTGGTCGG ACTCGGTTGG GCTCGGGCGG CCCC GCCTCC 250
CCCCGCCCGC CAGGCGGGCC CTTCTCGACG GCGCGGGGCG GGCCCTGCGG 300
GCGCGGGGCT GAAGGCGGAA CCACGACGGG CAGAGAGCAC GGAGCCGGGA 350
AGCCCCTGGG CGCCCGTCGG AGGGCTATGG AGCAGCGGCC GCGGGGCTGC 400
GCGGCGGTGG CGGCGGCGCT CCTCCTGGTG CTGCTGGGGG CCCGGGCCCA 450
GGGCGGCACT CGTAGCCCCA GGTGTGACTG TGCCGGTGAC TTCCACAAGA 500
AGATTGGTCT GTTTTGTTC AGAGGCTGCC CAGCGGGGCA CTACCTGAAG 550

GCCCCTTGCA CGGAGCCCTG CGGCAACTCC ACCTGCCTTG TGTGTCCCCA 600
 AGACACCTTC TTGGCCTGGG AGAACCACCA TAATTCTGAA TGTGCCCCT 650
 GCCAGGCCTG TGATGAGCAG GCCTCCCAGG TGGCGCTGGA GAACTGTTCA 700
 GCAGTGGCCG ACACCCGCTG TGGCTGTAAG CCAGGCTGGT TTGTGGAGTG 750
 CCAGGTCAGC CAATGTGTCA GCAGTTCACC CTTCTACTGC CAACCATGCC 800
 TAGACTGCGG GGCCCTGCAC CGCCACACAC GGCTACTCTG TTCCCGCAGA 850
 GATACTGACT GTGGGACCTG CCTGCCTGGC TTCTATGAAC ATGGCGATGG 900
 CTGCGTGTCC TGCCCCACGT AATTCTTAGC TGTCGTGGGA TGGAGGGAAG 950
 GGGCGCTGGG AGCAGAGCAG GGGCCTGGGG TGGGGCAGGT GCTGCTGGTT 1000
 CAGGAATAGG AAGAGGGGAT AGGGAGGAGG GAGCCTTGGC CCTGTGATGG 1050
 GTGGGCCCCA CTTCAGGCAA ACTTAGATGG CAAAAGAGCA ATCTGGATCC 1100
 GCCTTAGCCA GATACATAAG GGTATTTGCC TTCACCTTCA GCCAGCATTC 1150
 CCCCCAGCGA TCCTAGCCAG ATATTACAGA TGATTTGTCA CTTACACAGA 1200
 GAGTCACATT GATATAGCTT TAAAACTTGG GCTGAAGGAG GTTGAGGCTG 1250
 CAGTGAGCTA TGATCGTGCC ACTGCACTTC AGCCTGGGCA ACAGAGCGAG 1300
 ACCTATTAAA TAAATAAATA AATATTAAAT CTATTAAATA TTAAATATTA 1350
 AATCTATTAA ATAAATAAAT ACAAAGGGCT GAGAGTCAGG ACTGTGCTGC 1400
 TAGTTCTCTA GGGGATCTTG GGCAAGTGCA GAGAATTC 1438

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 417 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Gln	Arg	Pro	Arg	Gly	Cys	Ala	Ala	Val	Ala	Ala	Ala	Leu
1				5					10					15
Leu	Leu	Val	Leu	Leu	Gly	Ala	Arg	Ala	Gln	Gly	Gly	Thr	Arg	Ser
				20					25					30
Pro	Arg	Cys	Asp	Cys	Ala	Gly	Asp	Phe	His	Lys	Lys	Ile	Gly	Leu
				35					40					45
Phe	Cys	Cys	Arg	Gly	Cys	Pro	Ala	Gly	His	Tyr	Leu	Lys	Ala	Pro
				50					55					60
Cys	Thr	Glu	Pro	Cys	Gly	Asn	Ser	Thr	Cys	Leu	Val	Cys	Pro	Gln
				65					70					75
Asp	Thr	Phe	Leu	Ala	Trp	Glu	Asn	His	His	Asn	Ser	Glu	Cys	Ala
				80					85					90

Arg	Cys	Gln	Ala	Cys	Asp	Glu	Gln	Ala	Ser	Gln	Val	Ala	Leu	Glu	95	100	105
Asn	Cys	Ser	Ala	Val	Ala	Asp	Thr	Arg	Cys	Gly	Cys	Lys	Pro	Gly	110	115	120
Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	Gln	Cys	Val	Ser	Ser	Ser	Pro	125	130	135
Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	Gly	Ala	Leu	His	Arg	His	140	145	150
Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	Asp	Thr	Asp	Cys	Gly	Thr	Cys	155	160	165
Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys	Val	Ser	Cys	Pro	170	175	180
Thr	Ser	Thr	Leu	Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala	Ala	Val	Cys	185	190	195
Gly	Trp	Arg	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Ala	Gly	Leu	200	205	210
Val	Val	Pro	Leu	Leu	Leu	Gly	Ala	Thr	Leu	Thr	Tyr	Thr	Tyr	Arg	215	220	225
His	Cys	Trp	Pro	His	Lys	Pro	Leu	Val	Thr	Ala	Asp	Glu	Ala	Gly	230	235	240
Met	Glu	Ala	Leu	Thr	Pro	Pro	Pro	Ala	Thr	His	Leu	Ser	Pro	Leu	245	250	255
Asp	Ser	Ala	His	Thr	Leu	Leu	Ala	Pro	Pro	Asp	Ser	Ser	Glu	Lys	260	265	270
Ile	Cys	Thr	Val	Gln	Leu	Val	Gly	Asn	Ser	Trp	Thr	Pro	Gly	Tyr	275	280	285
Pro	Glu	Thr	Gln	Glu	Ala	Leu	Cys	Pro	Gln	Val	Thr	Trp	Ser	Trp	290	295	300
Asp	Gln	Leu	Pro	Ser	Arg	Ala	Leu	Gly	Pro	Ala	Ala	Ala	Pro	Thr	305	310	315
Leu	Ser	Pro	Glu	Ser	Pro	Ala	Gly	Ser	Pro	Ala	Met	Met	Leu	Gln	320	325	330
Pro	Gly	Pro	Gln	Leu	Tyr	Asp	Val	Met	Asp	Ala	Val	Pro	Ala	Arg	335	340	345
Arg	Trp	Lys	Glu	Phe	Val	Arg	Thr	Leu	Gly	Leu	Arg	Glu	Ala	Glu	350	355	360
Ile	Glu	Ala	Val	Glu	Val	Glu	Ile	Gly	Arg	Phe	Arg	Asp	Gln	Gln	365	370	375
Tyr	Glu	Met	Leu	Lys	Arg	Trp	Arg	Gln	Gln	Gln	Pro	Ala	Gly	Leu	380	385	390
Gly	Ala	Val	Tyr	Ala	Ala	Leu	Glu	Arg	Met	Gly	Leu	Asp	Gly	Cys	395	400	405

Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
 410 415

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCGCTCTGG TGGCCCTTGC AGAAGCC 27

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCGGCCGAG AAGTTGAGAA ATGTC 25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1634 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACCACGACG GGCAGAGAGC 50

ACGGAGCCGG GAAGCCCCTG GGCGCCCGTC GGAGGGCT ATG GAG 94
 Met Glu
 1

CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC 133
 Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
 5 10 15

CTC CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT 172
 Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr
 20 25

CGT AGC CCC AGG TGT GAC TGT GCC GGT GAC TTC CAC AAG 211
 Arg Ser Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys
 30 35 40

AAG ATT GGT CTG TTT TGT TGC AGA GGC TGC CCA GCG GGG 250
 Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala Gly
 45 50

CAC	TAC	CTG	AAG	GCC	CCT	TGC	ACG	GAG	CCC	TGC	GGC	AAC	289
His	Tyr	Leu	Lys	Ala	Pro	Cys	Thr	Glu	Pro	Cys	Gly	Asn	
55					60					65			
TCC	ACC	TGC	CTT	GTG	TGT	CCC	CAA	GAC	ACC	TTC	TTG	GCC	328
Ser	Thr	Cys	Leu	Val	Cys	Pro	Gln	Asp	Thr	Phe	Leu	Ala	
		70					75					80	
TGG	GAG	AAC	CAC	CAT	AAT	TCT	GAA	TGT	GCC	CGC	TGC	CAG	367
Trp	Glu	Asn	His	His	Asn	Ser	Glu	Cys	Ala	Arg	Cys	Gln	
				85					90				
GCC	TGT	GAT	GAG	CAG	GCC	TCC	CAG	GTG	GCG	CTG	GAG	AAC	406
Ala	Cys	Asp	Glu	Gln	Ala	Ser	Gln	Val	Ala	Leu	Glu	Asn	
	95					100					105		
TGT	TCA	GCA	GTG	GCC	GAC	ACC	CGC	TGT	GGC	TGT	AAG	CCA	445
Cys	Ser	Ala	Val	Ala	Asp	Thr	Arg	Cys	Gly	Cys	Lys	Pro	
			110					115					
GGC	TGG	TTT	GTG	GAG	TGC	CAG	GTC	AGC	CAA	TGT	GTC	AGC	484
Gly	Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	Gln	Cys	Val	Ser	
120					125					130			
AGT	TCA	CCC	TTC	TAC	TGC	CAA	CCA	TGC	CTA	GAC	TGC	GGG	523
Ser	Ser	Pro	Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	Gly	
		135					140					145	
GCC	CTG	CAC	CGC	CAC	ACA	CGG	CTA	CTC	TGT	TCC	CGC	AGA	562
Ala	Leu	His	Arg	His	Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	
				150					155				
GAT	ACT	GAC	TGT	GGG	ACC	TGC	CTG	CCT	GGC	TTC	TAT	GAA	601
Asp	Thr	Asp	Cys	Gly	Thr	Cys	Leu	Pro	Gly	Phe	Tyr	Glu	
	160					165					170		
CAT	GGC	GAT	GGC	TGC	GTG	TCC	TGC	CCC	ACG	AGC	ACC	CTG	640
His	Gly	Asp	Gly	Cys	Val	Ser	Cys	Pro	Thr	Ser	Thr	Leu	
			175					180					
GGG	AGC	TGT	CCA	GAG	CGC	TGT	GCC	GCT	GTC	TGT	GGC	TGG	679
Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala	Ala	Val	Cys	Gly	Trp	
185					190					195			
AGG	CAG	ATG	TTC	TGG	GTC	CAG	GTG	CTC	CTG	GCT	GGC	CTT	718
Arg	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Ala	Gly	Leu	
		200					205					210	
GTG	GTC	CCC	CTC	CTG	CTT	GGG	GCC	ACC	CTG	ACC	TAC	ACA	757
Val	Val	Pro	Leu	Leu	Leu	Gly	Ala	Thr	Leu	Thr	Tyr	Thr	
				215					220				
TAC	CGC	CAC	TGC	TGG	CCT	CAC	AAG	CCC	CTG	GTT	ACT	GCA	796
Tyr	Arg	His	Cys	Trp	Pro	His	Lys	Pro	Leu	Val	Thr	Ala	
	225					230					235		
GAT	GAA	GCT	GGG	ATG	GAG	GCT	CTG	ACC	CCA	CCA	CCG	GCC	835
Asp	Glu	Ala	Gly	Met	Glu	Ala	Leu	Thr	Pro	Pro	Pro	Ala	
			240					245					
ACC	CAT	CTG	TCA	CCC	TTG	GAC	AGC	GCC	CAC	ACC	CTT	CTA	874
Thr	His	Leu	Ser	Pro	Leu	Asp	Ser	Ala	His	Thr	Leu	Leu	
250					255					260			

GCA CCT CCT GAC AGC AGT GAG AAG ATC TGC ACC GTC CAG 913
Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys Thr Val Gln
265 270 275

TTG GTG GGT AAC AGC TGG ACC CCT GGC TAC CCC GAG ACC 952
Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr
280 285

CAG GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC 991
Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp
290 295 300

CAG TTG CCC AGC AGA GCT CTT GGC CCC GCT GCT GCG CCC 1030
Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro
305 310

ACA CTC TCG CCA GAG TCC CCA GCC GGC TCG CCA GCC ATG 1069
Thr Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met
315 320 325

ATG CTG CAG CCG GGC CCG CAG CTC TAC GAC GTG ATG GAC 1108
Met Leu Gln Pro Gly Pro Gln Leu Tyr Asp Val Met Asp
330 335 340

GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC ACG 1147
Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr
345 350

CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG 1186
Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val
355 360 365

GAG ATC GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC 1225
Glu Ile Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu
370 375

AAG CGC TGG CGC CAG CAG CAG CCC GCG GGC CTC GGA GCC 1264
Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu Gly Ala
380 385 390

GTT TAC GCG GCC CTG GAG CGC ATG GGG CTG GAC GGC TGC 1303
Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys
395 400 405

GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC CCG T 1340
Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
410 415 417

GACACGGCGC CCACTTGCCA CCTAGGCGCT CTGGTGGCCC TTGCAGAAGC 1390
CCTAAGTACG GTTACTTATG CGTGTAGACA TTTTATGTCA CTTATTAAGC 1440
CGCTGGCACG GCCCTGCGTA GCAGCACCAG CCGGCCCCAC CCCTGCTCGC 1490
CCCTATCGCT CCAGCCAAGG CGAAGAAGCA CGAACGAATG TCGAGAGGGG 1540
GTGAAGACAT TTCTCAACTT CTCGGCCGGA GTTTGGCTGA GATCGCGGTA 1590
TTAAATCTGT GAAAGAAAAC AAAAAAAAAA AAAAAAAAAA AAAA 1634

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Val	Cys	Pro	Gln	Gly	Lys	Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	Ile	1	5	10	15
Cys	Cys	Thr	Lys	Cys	His	Lys	Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	20	25	30	
Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser	Gly	35	40	45	
Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys	50	55	60	
Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	65	70	75	
Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	80	85	90	
Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	95	100	105	
Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	110	115	120	
Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	125	130	135	
Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	140	145	150	
Lys	Leu	Cys	Leu															

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Thr	Cys	Arg	Leu	Arg	Glu	Tyr	Tyr	Asp	Gln	Thr	Ala	Gln	Met	Cys	
1				5					10					15	
Cys	Ser	Lys	Cys	Ser	Pro	Gly	Gln	His	Ala	Lys	Val	Phe	Cys	Thr	
				20					25					30	
Lys	Thr	Ser	Asp	Thr	Val	Cys	Asp	Ser	Cys	Glu	Asp	Ser	Thr	Tyr	
				35					40					45	
Thr	Gln	Leu	Trp	Asn	Trp	Val	Pro	Glu	Cys	Leu	Ser	Cys	Gly	Ser	
				50					55					60	
Arg	Cys	Ser	Ser	Asp	Gln	Val	Glu	Thr	Gln	Ala	Cys	Thr	Arg	Glu	
				65					70					75	
Gln	Asn	Arg	Ile	Cys	Thr	Cys	Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Leu	
				80					85					90	
Ser	Lys	Gln	Glu	Gly	Cys	Arg	Leu	Cys	Ala	Pro	Leu	Arg	Lys	Cys	
				95					100					105	
Arg	Pro	Gly	Phe	Gly	Val	Ala	Arg	Pro	Gly	Thr	Glu	Thr	Ser	Asp	
				110					115					120	
Val	Val	Cys	Lys	Pro	Cys	Ala	Pro	Gly	Thr	Phe	Ser	Asn	Thr	Thr	
				125					130					135	
Ser	Ser	Thr	Asp	Ile	Cys	Arg	Pro	His	Gln	Ile	Cys	Asn	Val	Val	
				140					145					150	
Ala	Ile	Pro	Gly	Asn	Ala	Ser	Arg	Asp	Ala	Val	Cys	Thr			
				155					160						

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Thr	Cys	Arg	Asp	Gln	Glu	Lys	Glu	Tyr	Tyr	Glu	Pro	Gln	His	Arg	
1				5					10					15	
Ile	Cys	Cys	Ser	Arg	Cys	Pro	Pro	Gly	Thr	Tyr	Val	Ser	Ala	Lys	
				20					25					30	
Cys	Ser	Arg	Ile	Arg	Asp	Thr	Val	Cys	Ala	Thr	Cys	Ala	Glu	Asn	
				35					40					45	
Ser	Tyr	Asn	Glu	His	Trp	Asn	Tyr	Leu	Thr	Ile	Cys	Gln	Leu	Cys	
				50					55					60	

Arg	Pro	Cys	Asp	Pro	Val	Met	Gly	Leu	Glu	Glu	Ile	Ala	Pro	Cys	
				65					70					75	
Thr	Ser	Lys	Arg	Lys	Thr	Gln	Cys	Arg	Cys	Gln	Pro	Gly	Met	Phe	
				80					85					90	
Cys	Ala	Ala	Trp	Ala	Leu	Glu	Cys	Thr	His	Cys	Glu	Leu	Leu	Ser	
				95					100					105	
Asp	Cys	Pro	Pro	Gly	Thr	Glu	Ala	Glu	Leu	Lys	Asp	Glu	Val	Gly	
				110					115					120	
Lys	Gly	Asn	Asn	His	Cys	Val	Pro	Cys	Lys	Ala	Gly	His	Phe	Gln	
				125					130					135	
Asn	Thr	Ser	Ser	Pro	Ser	Ala	Arg	Cys	Gln	Pro	His	Thr	Arg	Cys	
				140					145					150	
Glu	Asn	Gln	Gly	Leu	Val	Glu	Ala	Ala	Pro	Gly	Thr	Ala	Gln	Ser	
				155					160					165	
Asp	Thr	Thr	Cys	Lys											
				170											

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn	Leu	Glu	Gly	Leu	His	His	Asp	Gly	Gln	Phe	Cys	His	Lys	Pro	
1				5					10					15	
Cys	Pro	Pro	Gly	Glu	Arg	Lys	Ala	Arg	Asp	Cys	Thr	Val	Asn	Gly	
				20					25					30	
Asp	Glu	Pro	Asp	Cys	Val	Pro	Cys	Gln	Glu	Gly	Lys	Glu	Tyr	Thr	
				35					40					45	
Asp	Lys	Ala	His	Phe	Ser	Ser	Lys	Cys	Arg	Arg	Cys	Arg	Leu	Cys	
				50					55					60	
Asp	Glu	Gly	His	Gly	Leu	Glu	Val	Glu	Ile	Asn	Cys	Thr	Arg	Thr	
				65					70					75	
Gln	Asn	Thr	Lys	Cys	Arg	Cys	Lys	Pro	Asn	Phe	Phe	Cys	Asn	Ser	
				80					85					90	
Thr	Val	Cys	Glu	His	Cys	Asp	Pro	Cys	Thr	Lys	Cys	Glu	His	Gly	
				95					100					105	
Ile	Ile	Lys	Glu	Cys	Thr	Leu	Thr	Ser	Asn	Thr	Lys	Cys	Lys		
				110					115						

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala	Cys	Pro	Thr	Gly	Leu	Tyr	Thr	His	Ser	Gly	Glu	Cys	Cys	Lys
1				5					10					15
Ala	Cys	Asn	Leu	Gly	Glu	Gly	Val	Ala	Gln	Pro	Cys	Gly	Ala	Asn
				20					25					30
Gln	Thr	Val	Cys	Glu	Pro	Cys	Leu	Asp	Ser	Val	Thr	Phe	Ser	Asp
				35					40					45
Val	Val	Ser	Ala	Thr	Glu	Pro	Cys	Lys	Pro	Cys	Thr	Glu	Cys	Val
				50					55					60
Gly	Leu	Gln	Ser	Met	Ser	Ala	Pro	Cys	Val	Glu	Ala	Asp	Asp	Ala
				65					70					75
Val	Cys	Arg	Cys	Ala	Tyr	Gly	Tyr	Tyr	Gln	Asp	Glu	Thr	Thr	Gly
				80					85					90
Arg	Cys	Glu	Ala	Cys	Arg	Val	Cys	Glu	Ala	Gly	Ser	Gly	Leu	Val
				95					100					105
Phe	Ser	Cys	Gln	Asp	Lys	Gln	Asn	Thr	Val	Cys	Glu	Glu	Cys	Pro
				110					115					120
Asp	Gly	Thr	Tyr	Ser	Asp	Glu	Ala	Asn	His	Val	Asp	Pro	Cys	Leu
				125					130					135
Pro	Cys	Thr	Val	Cys	Glu	Asp	Thr	Glu	Arg	Gln	Leu	Arg	Glu	Cys
				140					145					150
Thr	Arg	Trp	Ala	Asp	Ala	Glu	Cys	Glu						
				155										

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ala	Cys	Arg	Glu	Lys	Gln	Tyr	Leu	Ile	Asn	Ser	Gln	Cys	Cys	Ser
1				5					10					15
Leu	Cys	Gln	Pro	Gly	Gln	Lys	Leu	Val	Ser	Asp	Cys	Thr	Glu	Phe
				20					25					30
Thr	Glu	Thr	Glu	Cys	Leu	Pro	Cys	Gly	Glu	Ser	Glu	Phe	Leu	Asp
				35					40					45
Thr	Trp	Asn	Arg	Glu	Thr	His	Cys	His	Gln	His	Lys	Tyr	Cys	Asp
				50					55					60
Pro	Asn	Leu	Gly	Leu	Arg	Val	Gln	Gln	Lys	Gly	Thr	Ser	Glu	Thr
				65					70					75
Asp	Thr	Ile	Cys	Thr	Cys	Glu	Glu	Gly	Trp	His	Cys	Thr	Ser	Glu
				80					85					90

Ala	Cys	Glu	Ser	Cys	Val	Leu	His	Arg	Ser	Cys	Ser	Pro	Gly	Phe
				95					100					105
Gly	Val	Lys	Gln	Ile	Ala	Thr	Gly	Val	Ser	Asp	Thr	Ile	Cys	Glu
				110					115					120
Pro	Cys	Pro	Val	Gly	Phe	Phe	Ser	Asn	Val	Ser	Ser	Ala	Phe	Glu
				125					130					135
Lys	Cys	His	Pro	Trp	Thr	Ser	Cys	Glu	Thr	Lys	Asp	Leu	Val	Val
				140					145					150
Gln	Gln	Ala	Gly	Thr	Asn	Lys	Thr	Asp	Val	Val	Cys	Gly		
				155					160					

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ser	Cys	Pro	Glu	Arg	His	Tyr	Trp	Ala	Gln	Gly	Lys	Leu	Cys	Cys
1				5					10					15
Gln	Met	Cys	Glu	Pro	Gly	Thr	Phe	Leu	Val	Lys	Asp	Cys	Asp	Gln
				20					25					30
His	Arg	Lys	Ala	Ala	Gln	Cys	Asp	Pro	Cys	Ile	Pro	Gly	Val	Ser
				35					40					45
Phe	Ser	Pro	Asp	His	His	Thr	Arg	Pro	His	Cys	Glu	Ser	Cys	Arg
				50					55					60
His	Cys	Asn	Ser	Gly	Leu	Leu	Val	Arg	Asn	Cys	Thr	Ile	Thr	Ala
				65					70					75
Asn	Ala	Glu	Cys	Ala	Cys	Arg	Asn	Gly	Trp	Gln	Cys	Arg	Asp	Lys
				80					85					90
Glu	Cys	Thr	Glu	Cys	Asp	Pro	Leu	Pro	Asn	Pro	Ser	Leu	Thr	Ala
				95					100					105
Arg	Ser	Ser	Gln	Ala	Leu	Ser	Pro	His	Pro	Gln	Pro	Thr	His	Leu
				110					115					120
Pro														

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Thr	Cys	His	Gly	Asn	Pro	Ser	His	Tyr	Tyr	Asp	Lys	Ala	Val	Arg
1				5					10					15

Arg	Cys	Cys	Tyr	Arg	Cys	Pro	Met	Gly	Leu	Phe	Pro	Thr	Gln	Gln	
				20					25					30	
Cys	Pro	Gln	Arg	Pro	Thr	Asp	Cys	Arg	Lys	Gln	Cys	Glu	Pro	Asp	
				35					40					45	
Tyr	Tyr	Leu	Asp	Glu	Ala	Asp	Arg	Cys	Thr	Ala	Cys	Val	Thr	Cys	
				50					55					60	
Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr	Pro	Cys	Ala	Trp	Asn	Ser	
				65					70					75	
Ser	Arg	Val	Cys	Glu	Cys	Arg	Pro	Gly	Met	Phe	Cys	Ser	Thr	Ser	
				80					85					90	
Ala	Val	Asn	Ser	Cys	Ala	Arg	Cys	Phe	Phe	His	Ser	Val	Cys	Pro	
				95					100					105	
Ala	Gly	Met	Ile	Val	Lys	Phe	Pro	Gly	Thr	Ala	Gln	Lys	Asn	Thr	
				110					115					120	
Val	Cys	Glu													

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

His	Cys	Val	Gly	Asp	Thr	Tyr	Pro	Ser	Asn	Asp	Arg	Cys	Cys	His	
1				5					10					15	
Glu	Cys	Arg	Pro	Gly	Asn	Gly	Met	Val	Ser	Arg	Cys	Ser	Arg	Ser	
				20					25					30	
Gln	Asn	Thr	Val	Cys	Arg	Pro	Cys	Gly	Pro	Gly	Phe	Tyr	Asn	Asp	
				35					40					45	
Val	Val	Ser	Ser	Lys	Pro	Cys	Lys	Pro	Cys	Thr	Trp	Cys	Asn	Leu	
				50					55					60	
Arg	Ser	Gly	Ser	Glu	Arg	Lys	Gln	Leu	Cys	Thr	Ala	Thr	Gln	Asp	
				65					70					75	
Thr	Val	Cys	Arg	Cys	Arg	Ala	Gly	Thr	Gln	Pro	Leu	Asp	Ser	Tyr	
				80					85					90	
Lys	Pro	Gly	Val	Asp	Cys	Ala	Pro	Cys	Pro	Pro	Gly	His	Phe	Ser	
				95					100					105	
Pro	Gly	Asp	Asn	Gln	Ala	Cys	Lys	Pro	Trp	Thr	Asn	Cys	Thr	Leu	
				110					115					120	
Ala	Gly	Lys	His	Thr	Leu	Gln	Pro	Ala	Ser	Asn	Ser	Ser	Asp	Ala	
				125					130					135	
Ile	Cys	Glu													

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 amino acids
(B) TYPE: PRT
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Gly	Leu	Ser	Thr	Val	Pro	Asp	Leu	Leu	Leu	Pro	Leu	Val	Leu	
1				5					10					15	
Leu	Glu	Leu	Leu	Val	Gly	Ile	Tyr	Pro	Ser	Gly	Val	Ile	Gly	Leu	
				20					25					30	
Val	Pro	His	Leu	Gly	Asp	Arg	Glu	Lys	Arg	Asp	Ser	Val	Cys	Pro	
				35					40					45	
Gln	Gly	Lys	Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	Ile	Cys	Cys	Thr	
				50					55					60	
Lys	Cys	His	Lys	Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	Pro	Gly	Pro	
				65					70					75	
Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	
				80					85					90	
Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	Cys	
				95					100					105	
Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	
				110					115					120	
Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His	Tyr	
				125					130					135	
Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu	Cys	Leu	
				140					145					150	
Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val	
				155					160					165	
Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val	
				170					175					180	
Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	Lys	Leu	Cys	
				185					190					195	
Leu	Pro														

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 amino acids
(B) TYPE: PRT
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Leu	Gly	Ile	Trp	Thr	Leu	Leu	Pro	Leu	Val	Leu	Thr	Ser	Val	
1				5					10					15	

Ala	Arg	Leu	Ser	Ser	Lys	Ser	Val	Asn	Ala	Gln	Val	Thr	Asp	Ile	
				20					25					30	
Asn	Ser	Lys	Gly	Leu	Glu	Leu	Arg	Lys	Thr	Val	Thr	Thr	Val	Glu	
				35					40					45	
Thr	Gln	Asn	Leu	Glu	Gly	Leu	His	His	Asp	Gly	Gln	Phe	Cys	His	
				50					55					60	
Lys	Pro	Cys	Pro	Pro	Gly	Glu	Arg	Lys	Ala	Arg	Asp	Cys	Thr	Val	
				65					70					75	
Asn	Gly	Asp	Glu	Pro	Asp	Cys	Val	Pro	Cys	Gln	Glu	Gly	Lys	Glu	
				80					85					90	
Tyr	Thr	Asp	Lys	Ala	His	Phe	Ser	Ser	Lys	Cys	Arg	Arg	Cys	Arg	
				95					100					105	
Leu	Cys	Asp	Glu	Gly	His	Gly	Leu	Glu	Val	Glu	Ile	Asn	Cys	Thr	
				110					115					120	
Arg	Thr	Gln	Asn	Thr	Lys	Cys	Arg	Cys	Lys	Pro	Asn	Phe	Phe	Cys	
				125					130					135	
Asn	Ser	Thr	Val	Cys	Glu	His	Cys	Asp	Pro	Cys	Thr	Lys	Cys	Glu	
				140					145					150	
His	Gly	Ile	Ile	Lys	Glu	Cys	Thr	Leu	Thr	Ser	Asn	Thr	Lys	Cys	
				155					160					165	

Lys Glu

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: PRT
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Val	Val	Glu	Asn	Val	Pro	Pro	Leu	Arg	Trp	Lys	Glu	Phe	Val	Arg	
1				5					10					15	
Arg	Leu	Gly	Leu	Ser	Asp	His	Glu	Ile	Asp	Arg	Leu	Glu	Leu	Gln	
				20					25					30	
Asn	Gly	Arg	Cys	Leu	Arg	Glu	Ala	Gln	Tyr	Ser	Met	Leu	Ala	Thr	
				35					40					45	
Trp	Arg	Arg	Arg	Thr	Pro	Arg	Arg	Glu	Ala	Thr	Leu	Glu	Leu	Leu	
				50					55					60	
Gly	Arg	Val	Leu	Arg	Asp	Met	Asp	Leu	Leu	Gly	Cys	Leu	Glu	Asp	
				65					70					75	

Ile Glu Glu

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids
 (B) TYPE: PRT
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ile	Ala	Gly	Val	Met	Thr	Leu	Ser	Gln	Val	Lys	Gly	Phe	Val	Arg
1				5					10					15
Lys	Asn	Gly	Val	Asn	Glu	Ala	Lys	Ile	Asp	Glu	Ile	Lys	Asn	Asp
				20					25					30
Asn	Val	Gln	Asp	Thr	Ala	Glu	Gln	Lys	Val	Gln	Leu	Leu	Arg	Asn
				35					40					45
Trp	His	Gln	Leu	His	Gly	Lys	Lys	Glu	Ala	Tyr	Asp	Thr	Leu	Ile
				50					55					60
Lys	Asp	Leu	Lys	Lys	Ala	Asn	Leu	Cys	Thr	Leu	Ala	Glu	Lys	Ile
				65					70					75

Gln Thr

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 amino acids
 (B) TYPE: PRT
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ile	Cys	Asp	Asn	Val	Gly	Lys	Asp	Trp	Arg	Arg	Leu	Ala	Arg	Gln
1				5					10					15
Leu	Lys	Val	Ser	Asp	Thr	Lys	Ile	Asp	Ser	Ile	Glu	Asp	Arg	Tyr
				20					25					30
Pro	Arg	Asn	Leu	Thr	Glu	Arg	Val	Arg	Glu	Ser	Leu	Arg	Ile	Trp
				35					40					45
Lys	Asn	Thr	Glu	Lys	Glu	Asn	Ala	Thr	Val	Ala	His	Leu	Val	Gly
				50					55					60
Ala	Leu	Arg	Ser	Cys	Gln	Met	Asn	Leu	Val	Ala	Asp	Leu	Val	
				65					70					

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: PRT
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Asn	Arg	Pro	Leu	Ser	Leu	Lys	Asp	Gln	Gln	Thr	Phe	Ala	Arg	Ser
1				5					10					15
Val	Gly	Leu	Lys	Trp	Arg	Lys	Val	Gly	Arg	Ser	Leu	Gln	Arg	Gly
				20					25					30

Cys Arg Ala Leu Arg Asp Pro Ala Leu Asp Ser Leu Ala Tyr Glu
 35 40 45
 Tyr Glu Arg Glu Gly Leu Tyr Glu Gln Ala Phe Gln Leu Leu Arg
 50 55 60
 Arg Phe Val Gln Ala Glu Gly Arg Arg Ala Thr Leu Gln Arg Leu
 65 70 75
 Val Glu

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: PRT
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ile Arg Glu Asn Leu Gly Lys His Trp Lys Asn Cys Ala Arg Lys
 1 5 10 15
 Leu Gly Phe Thr Gln Ser Gln Ile Asp Glu Ile Asp His Asp Tyr
 20 25 30
 Glu Arg Asp Gly Leu Lys Glu Lys Val Tyr Gln Met Leu Gln Lys
 35 40 45
 Trp Val Met Arg Glu Gly Ile Lys Gly Ala Thr Val Gly Lys Leu
 50 55 60
 Ala Gln Ala Leu His Gln Cys Ser Arg Ile Asp Leu Leu Ser Ser
 65 70 75
 Leu Thr

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: PRT
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Ala Val Ala Phe Tyr Ile Pro Asp Gln Ala Thr Leu Leu Arg
 1 5 10 15
 Glu Ala Glu Gln Lys Glu Gln Gln Ile Leu Arg Leu Arg Glu Ser
 20 25 30
 Gln Trp Arg Phe Leu Ala Thr Val Val Leu Glu Thr Leu Lys Gln
 35 40 45
 Tyr Thr Ser Cys His Pro Lys Thr Gly Arg Lys Ser Gly Lys Tyr
 50 55 60
 Arg Lys Pro